

```

11      5' TG CAG CAG AGG GAG ACC CGC GGC AAC CCC GGC AAC CCA GGC CTC GGC GTC GCT 56
        65      74      83      92      101      110
GCC ACC ATG ACG GGA AGC AAT ATG TCG GAC GCC TTG GCC AAC GCC GTG TGC CAG
M T G S N M S D A L A N A V C Q

119      128      137      146      155      164
CGC TGC CAG GCC CGC TTC TCC CCC GGC GAG CGC ATT GTC AAC AGC AAT GGC GAG
R C Q A R F S P A E R I V N S N G E

173      182      191      200      209      218
CTG TAC CAT GAG CAC TGC TTC GTG TGT GCC CAG TGC TTC CGG CCC TTC CCC GAG
L Y H E H C F V C A Q C F R P F P E

227      236      245      254      263      272
GGG CTC TTC TAT GAG TTT GAA GGC CGG AAG TAC TGC GAA CAC GAC TTC CAA ATG
G L F Y E F E G R K Y C E H D F Q M

281      290      299      308      317      326
CTG TTT GCT CCG TGC TGT GGA TCC TGC GGT GAG TTC ATC ATC ATT GGC CGC GTC ATC
L F A P C C G S C G E F I I G R V I

335      344      353      362      371      380
AAG GCC ATG AAC AAC TGG CAC CCG GGC TGC TTC CGC TGC GAG CTG TGT GAT
K A M N N N W H P G C F R C E L C D

```

FIGURE 1A

389	398	407	416	425	434
GTG GAG CTG GCT GAC CTG GGC TTT GTG AAG AAT GCC GGC AGG CAT CTC TGC CGG	V E L A D L L G G F V V K N A A G G R H L C R				
443	452	461	470	479	488
CCT TGC CAC AAC CGT GAG AAG GCC AAG GGC CTG GGC AAG TAC ATC TGC CAG CGG	P C H N R E K A A K G L G K Y I C Q R				
497	506	515	524	533	542
TGC CAC CTG GTC ATC GAC GAG CAG CCC CTC ATG TTC AGG AGC GAC GCC TAC CAC	C H L V I D E Q P L M F R S D A Y H				
551	560	569	578	587	596
CCT GAC CAC TTC AAC TGC ACC CAC TGT TGT GGG AAG GAG CTG ACA GGC GAG GCC CGC	P D H F N C T H C C C C G K E L T A E A R				
605	614	623	632	641	650
GAG CTG AAG GGT GAG CTC TAC TGC CTG CCC TGC CAT GAC AAG ATG GGC GTC CCC	E L K G G E L Y C C L C P C H D K M G V P				
659	668	677	686	695	704
ATC TGC GGG GCC TGC CGC CGG CCC ATC GAG GGC CGA GTG GTC AAC GCG CTG GGC	I C G A C R R P I E G R V V N A L G				
713	722	731	740	749	758
AAG CAG TGG CAC GTG GAG CAC TTT GTC TGT GCC AAG TGT GAG AAG CCA TTC CTG	K Q W H V E H F V C A K K C E K P F L				

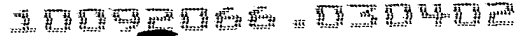
**FIGURE 1B**

[illegible]

FIGURE 1C

1145	1154	1163	1172	1181	1190
GCT GTC CAT GCT TGG CCC CCT CGT CCC CAT CCA CCT GTG CCC TCC GCA TCT TAC					
1199	1208	1217	1226	1235	1244
CCT CCC TTT CTC TTT CCT CAT TGC CTT CTC CCT TCC TGT TCC CTC ATC TCT GCC					
1253	1262	1271	1280	1289	1298
TTC CCC ATG TCT CTC CTC TCC TTG GCC GTG GCT TCT GTC TGT GAG GAG GCA GGA					
1307	1316	1325	1334	1343	1352
GCT GGG GAG TGG GAG CCT ATG ACC CCA CGT CTG ACA GCC ATG TCC ACC TGT GCC					
1361	1370	1379	1388	1397	1406
CAC AGC TTC CGC CCA CAG ACC TCC AGG GAC AGG AGC AAA TTG CAC CAC AGC TCC					
1415	1424	1433	1442	1451	1460
CCG CCT GGC CTG GCC CTC CCC AGG CGG CTC AGT GGC TCA TGC TGT CCT GTG AGA					
1469	1478	1487	1496	1505	1514
GCC CCT GCC CCA GAG CGG CCC CAC TAA GCG CAT GTG GCT CCT GGG CTA CCC ACA					
1523	1532	1541	1550	1559	1568
GCC AGG GCA GCC TGC TGG AGC CAC AGG GCC AGG GCC ATG CAG ATG GAG GCC TCT					
1577	1586	1595	1604	1613	1622
GGG AGC CAC CTC CAA TCC CTC ACC ACT CAC TCA ACC AGT GGC ACA GTG TCC TTG					
1631	1640	1649	1658	1667	1676
TGC CCA CAC TGA GCC AGC AAG TCC TGC TGT CCA CAC CCA GCT ACC TGG AGG					

FIGURE 1D



1685	1694	1703	1712	1721	1730
GAC AGG ACC CAC CTC CAT CCT TCG GAA GGC CTT CCT GGA ATC CCA CCT TGG CCT					
1739	1748	1757	1766	1775	1784
CCG CCC TCG GTT CCG CCC CGC CCC TCT CCC CCC GAC CTT GGG GCT TGT GTC GAG					
1793	1802	1811	1820	1829	1838
CCC TTG GGT GGG GCC AGG AGG AGG TGA TGG CGT CAG AGG AGG TGT GGT CAG AGG					
1847	1856	1865	1874	1883	1892
TGA CTT GTT CCC ACC TCC AGG GAG GAC GCT TCG TCT TCG GCC AGC GCA GAC CTG					
1901	1910	1919	1928	1937	1946
GTG TTT GTT TGT TTG TTG GGT CAC GCT TGC ACA ATG AAG GCT TGT TCA CAC AAA					
1955					
AAA AAA AAA AAA A 3					

FIGURE 1E

1	M	T	G	S	N	M	S	D	A	L	A	N	A	V	C	Q	R	C	Q	A	R	F	S	P	A	E	R	I	V	N	3540806
1	-	-	-	-	-	M	A	N	A	L	A	S	A	T	C	E	R	C	K	G	G	F	A	P	A	E	K	I	V	N	GI 516012
31	S	N	G	E	L	Y	H	E	H	C	F	V	C	A	Q	C	F	R	P	F	P	E	G	L	F	Y	E	F	E	G	3540806
26	S	N	G	E	L	Y	H	E	Q	C	F	V	C	A	Q	C	F	Q	Q	F	P	E	G	L	F	Y	E	F	E	G	GI 516012
61	R	K	Y	C	E	H	D	F	Q	M	L	F	A	P	C	C	G	S	C	G	E	F	I	I	G	R	V	I	K	A	3540806
56	R	K	Y	C	E	H	D	F	Q	M	L	F	A	P	C	C	H	Q	C	G	E	F	I	I	G	R	V	I	K	A	GI 516012
91	M	N	N	W	H	P	G	C	F	R	C	E	L	C	D	V	E	L	A	D	L	G	F	V	K	N	A	G	R	3540806	
86	M	N	N	S	W	H	P	E	C	F	R	C	D	L	C	Q	E	V	L	A	D	I	G	F	V	K	N	A	G	R	GI 516012
121	H	L	C	R	P	C	H	N	R	E	K	A	K	G	L	G	K	Y	I	C	Q	R	C	H	L	V	I	D	E	Q	3540806
116	H	L	C	R	P	C	H	N	R	E	K	A	R	G	L	G	K	Y	I	C	Q	K	C	H	A	I	I	D	E	Q	GI 516012
151	P	L	M	F	R	S	D	A	Y	H	P	D	H	F	N	C	T	H	C	G	K	E	L	T	A	E	A	R	E	L	3540806
146	P	L	I	F	K	N	D	P	Y	H	P	D	H	F	N	C	A	N	C	G	K	E	L	T	A	D	A	R	E	L	GI 516012
181	K	G	E	L	Y	C	L	P	C	H	D	K	M	G	V	P	I	C	G	A	C	R	R	P	I	E	G	R	V	V	3540806
176	K	G	E	L	Y	C	L	P	C	H	D	K	M	G	V	P	I	C	G	A	C	R	R	P	I	E	G	R	V	V	GI 516012
211	N	A	L	G	K	Q	W	H	V	E	H	F	V	C	A	K	C	E	K	P	F	L	G	H	R	H	Y	E	K	K	3540806
206	N	A	M	G	K	Q	W	H	V	E	H	F	V	C	A	K	C	E	K	P	F	L	G	H	R	H	Y	E	R	K	GI 516012
241	G	L	A	Y	C	E	T	H	Y	N	Q	L	F	G	D	V	C	Y	N	C	S	H	V	I	E	G	D	V	V	S	3540806
236	G	L	A	Y	C	E	T	H	Y	N	Q	L	F	G	D	V	C	F	H	C	N	R	V	I	E	G	D	V	V	S	GI 516012

FIGURE 2A

10050066.030402

271	A	L	N	K	A	W	C	V	S	C	F	S	C	S	T	C	N	S	K	L	T	L	K	N	K	F	V	E	F	D	3540806
266	A	L	N	K	A	W	C	V	N	C	F	A	C	S	T	C	N	T	K	L	T	L	K	N	K	F	V	E	F	D	GI 516012
301	M	K	P	V	C	K	R	C	Y	E	K	F	P	L	E	L	K	K	R	L	K	K	L	S	E	L	T	S	R	K	3540806
296	M	K	P	V	C	K	K	C	Y	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	S	I	G	GI 516012
331	A	Q	P	K	A	T	D	L	N	S	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3540806
310	A	E	E	K	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 516012

FIGURE 2B

<110> Lal, Preeti  
Guegler, Karl J.  
Corley, Neil C.

<120> ANTIBODY SPECIFICALLY BINDING HUMAN PINCH PROTEIN HOMOLOG

<130> PF-0460-2CIP

<140> To Be Assigned

<141> Herewith

<150> 09/528,959; 09/008,465

<151> 2000-03-20; 1998-01-16

<160> 3

<170> PERL Program

<210> 1

<211> 341

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Incyte ID No: 3540806CD1

<400> 1

Met	Thr	Gly	Ser	Asn	Met	Ser	Asp	Ala	Leu	Ala	Asn	Ala	Val	Cys
1				5					10					15
Gln	Arg	Cys	Gln	Ala	Arg	Phe	Ser	Pro	Ala	Glu	Arg	Ile	Val	Asn
			20						25					30
Ser	Asn	Gly	Glu	Leu	Tyr	His	Glu	His	Cys	Phe	Val	Cys	Ala	Gln
			35						40					45
Cys	Phe	Arg	Pro	Phe	Pro	Glu	Gly	Leu	Phe	Tyr	Glu	Phe	Glu	Gly
			50						55					60
Arg	Lys	Tyr	Cys	Glu	His	Asp	Phe	Gln	Met	Leu	Phe	Ala	Pro	Cys
			65						70					75
Cys	Gly	Ser	Cys	Gly	Glu	Phe	Ile	Ile	Gly	Arg	Val	Ile	Lys	Ala
			80						85					90
Met	Asn	Asn	Asn	Trp	His	Pro	Gly	Cys	Phe	Arg	Cys	Glu	Leu	Cys
			95						100					105
Asp	Val	Glu	Leu	Ala	Asp	Leu	Gly	Phe	Val	Lys	Asn	Ala	Gly	Arg
			110						115					120
His	Leu	Cys	Arg	Pro	Cys	His	Asn	Arg	Glu	Lys	Ala	Lys	Gly	Leu
			125						130					135
Gly	Lys	Tyr	Ile	Cys	Gln	Arg	Cys	His	Leu	Val	Ile	Asp	Glu	Gln
			140						145					150
Pro	Leu	Met	Phe	Arg	Ser	Asp	Ala	Tyr	His	Pro	Asp	His	Phe	Asn
			155						160					165
Cys	Thr	His	Cys	Gly	Lys	Glu	Leu	Thr	Ala	Glu	Ala	Arg	Glu	Leu
			170						175					180
Lys	Gly	Glu	Leu	Tyr	Cys	Leu	Pro	Cys	His	Asp	Lys	Met	Gly	Val
			185						190					195
Pro	Ile	Cys	Gly	Ala	Cys	Arg	Arg	Pro	Ile	Glu	Gly	Arg	Val	Val
			200						205					210
Asn	Ala	Leu	Gly	Lys	Gln	Trp	His	Val	Glu	His	Phe	Val	Cys	Ala
			215						220					225
Lys	Cys	Glu	Lys	Pro	Phe	Leu	Gly	His	Arg	His	Tyr	Glu	Lys	Lys



	230		235		240
Gly Leu Ala Tyr	Cys Glu Thr His Tyr	Asn Gln Leu Phe Gly	Asp		
	245		250		255
Val Cys Tyr Asn	Cys Ser His Val Ile	Glu Gly Asp Val Val	Ser		
	260		265		270
Ala Leu Asn Lys	Ala Trp Cys Val Ser	Cys Phe Ser Cys Ser	Thr		
	275		280		285
Cys Asn Ser Lys	Leu Thr Leu Lys Asn	Lys Phe Val Glu Phe	Asp		
	290		295		300
Met Lys Pro Val	Cys Lys Arg Cys Tyr	Glu Lys Phe Pro Leu	Glu		
	305		310		315
Leu Lys Lys Arg	Leu Lys Lys Leu Ser	Glu Leu Thr Ser Arg	Lys		
	320		325		330
Ala Gln Pro Lys	Ala Thr Asp Leu Asn	Ser Ala			
	335		340		

&lt;210&gt; 2

&lt;211&gt; 1959

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: 3540806CB1

&lt;400&gt; 2

```

tgcagcagca gagggagacc cgcggaacc cgggcaacc agggctcggc gtcgctgcca 60
ccatgacggg aagcaatatg tcggacgcct tggccaacgc cgtgtgccag cgctgccagg 120
cccgtttctc ccccgccgag cgcattgtca acagcaatgg ggagctgtac catgagcact 180
gcttcgtgtg tgcccagtgc ttccggccct tccccgaggg gctcttctat gagtttgaag 240
gccggaagta ctgcgaacac gacttccaaa tgctgtttgc tccgtgctgt ggatcctgcg 300
gtgagttcat cattggccgc gtcatcaagg ccatgaacaa caactggcac ccgggctgct 360
tccgctgcga gctgtgtgat gtggagctgg ctgacctggg ctttgtgaag aatgccggca 420
ggcatctctg ccggccttgc cacaaccgtg agaaggccaa gggcctgggc aagtacatct 480
gccagcgggt ccacctggtc atcgacgagc agccctcat gttcaggagc gacgcctacc 540
accctgacca cttcaactgc acccaactgt ggaaggagct gacagccgag gcccgcgagc 600
tgaaggggtg gctctactgc ctgccctgcc atgacaagat gggcgctccc atctgcgggg 660
cctgccgccc gcccatcgag ggccgagtg tcaacgcgct gggcaagcag tggcacgtgg 720
agcactttgt ctgtgccaag tgtgagaagc cattcctggg gcaccggcac tatgagaaga 780
agggcctggc ctactgagag actcactaca accagctctt cggggacgct tgctacaact 840
gcagccatgt gattgaaggc gatgtggtgt cggccctcaa caaggcctgg tgtgtgagct 900
gcttctcctg ctccacctgc aacagcaagc tcaccctgaa gaacaagttt gtggagtctc 960
acatgaagcc cgtgtgtaag aggtgctacg agaagttccc gctggagctg aagaagcggc 1020
tgaagaagct gtcggagctg acctcccgcg agggccagcc caaggccaca gacctcaact 1080
ctgcctgaag gccctcttgc gcactgcctc tcggcccctc cgccctctcc cctcctgctg 1140
tccatgcttg gcccctcgt ccccatccac ctgtgccctc cgcatcttac cctccccttc 1200
tctttcctca ttgccttctc ccttctgtgt cctcatctc tgccctcccc atgtctctcc 1260
tctccttggc cgtggcttct gtctgtgagg aggcaggagc tggggagtgg gacccatga 1320
ccccacgtct gacagccatg tccacctgtg cccacagctt ccgcccacag acctccaggg 1380
acaggagcaa attgcaccac agtccccgc ctggcctggc cctcccaggg cggctcagtg 1440
gctcatgctg tctgtgaga gccctgccc cagagcggcc ccactaagcg catgtggctc 1500
ctgggctacc cacagccagg gcagcctgct ggagccacag ggccaggggc atgcagatgg 1560
aggcctctgg gagccacctc caatccctca ccaactcctc aaccagtggc acagtgtcct 1620
tgtgccaca ctgagccagc aagtcctgct gtccacaccc acaagctacc tggaggggaca 1680
ggaccacact ccattcctcg gaaggccttc ctggaatccc accttggcct ccgcccctcg 1740
ttccgccccg cccctctccc cccgacctg gggttgtgt cgagcccttg ggtggggcca 1800
ggaggaggtg atggcgtagc aggaggtgtg gtcagaggtg acttgttccc acctccaggg 1860
aggacgcttc gtcttcggcc agcgcagacc tgggtgttgt ttgtttgttg ggtcacgctt 1920

```

PF-0460-2 CIP

gcacaatgaa ggcttggttca cacaaaaaaaa aaaaaaaaaa

1959

&lt;210&gt; 3

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;300&gt;

&lt;308&gt; Genbank ID No: g516012

&lt;400&gt; 3

Met	Ala	Asn	Ala	Leu	Ala	Ser	Ala	Thr	Cys	Glu	Arg	Cys	Lys	Gly	1	5	10	15
Gly	Phe	Ala	Pro	Ala	Glu	Lys	Ile	Val	Asn	Ser	Asn	Gly	Glu	Leu	20	25	30	35
Tyr	His	Glu	Gln	Cys	Phe	Val	Cys	Ala	Gln	Cys	Phe	Gln	Gln	Phe	40	45	50	55
Pro	Glu	Gly	Leu	Phe	Tyr	Glu	Phe	Glu	Gly	Arg	Lys	Tyr	Cys	Glu	60	65	70	75
His	Asp	Phe	Gln	Met	Leu	Phe	Ala	Pro	Cys	Cys	His	Gln	Cys	Gly	80	85	90	95
Glu	Phe	Ile	Ile	Gly	Arg	Val	Ile	Lys	Ala	Met	Asn	Asn	Ser	Trp	100	105	110	115
His	Pro	Glu	Cys	Phe	Arg	Cys	Asp	Leu	Cys	Gln	Glu	Val	Leu	Ala	120	125	130	135
Asp	Ile	Gly	Phe	Val	Lys	Asn	Ala	Gly	Arg	His	Leu	Cys	Arg	Pro	140	145	150	155
Cys	His	Asn	Arg	Glu	Lys	Ala	Arg	Gly	Leu	Gly	Lys	Tyr	Ile	Cys	160	165	170	175
Gln	Lys	Cys	His	Ala	Ile	Ile	Asp	Glu	Gln	Pro	Leu	Ile	Phe	Lys	180	185	190	195
Asn	Asp	Pro	Tyr	His	Pro	Asp	His	Phe	Asn	Cys	Ala	Asn	Cys	Gly	200	205	210	215
Lys	Glu	Leu	Thr	Ala	Asp	Ala	Arg	Glu	Leu	Lys	Gly	Glu	Leu	Tyr	220	225	230	235
Cys	Leu	Pro	Cys	His	Asp	Lys	Met	Gly	Val	Pro	Ile	Cys	Gly	Ala	240	245	250	255
Cys	Arg	Arg	Pro	Ile	Glu	Gly	Arg	Val	Val	Asn	Ala	Met	Gly	Lys	260	265	270	275
Gln	Trp	His	Val	Glu	His	Phe	Val	Cys	Ala	Lys	Cys	Glu	Lys	Pro	280	285	290	295
Phe	Leu	Gly	His	Arg	His	Tyr	Glu	Arg	Lys	Gly	Leu	Ala	Tyr	Cys	300	305	310	
Glu	Thr	His	Tyr	Asn	Gln	Leu	Phe	Gly	Asp	Val	Cys	Phe	His	Cys				
Asn	Arg	Val	Ile	Glu	Gly	Asp	Val	Val	Ser	Ala	Leu	Asn	Lys	Ala				
Trp	Cys	Val	Asn	Cys	Phe	Ala	Cys	Ser	Thr	Cys	Asn	Thr	Lys	Leu				
Thr	Leu	Lys	Asn	Lys	Phe	Val	Glu	Phe	Asp	Met	Lys	Pro	Val	Cys				
Lys	Lys	Cys	Tyr	Glu	Ile	Ser	Ile	Gly	Ala	Glu	Glu	Lys	Thr					